SEQUENCE LISTING

<110> BASF Aktiengesellschaft

<120> The N-terminal β-barrel structure of lipid body
      lipoxygenase mediates its binding to liposomes and
      lipid bodies [sic]

<130> 99_1235

<140>
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<170> PatentIn Vers. 2.0

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gga gat ctt gca ggt tct gtt atc aat gct ggt ggt aac att tta gat   96
Gly Asp Leu Ala Gly Ser Val Ile Asn Ala Gly Gly Asn Ile Leu Asp
            20   25   30

aga gtt tcc agt ctt gga gga aac aaa atc aaa ggg aaa gtg att ctt   144
Arg Val Ser Ser Leu Gly Gly Asn Lys Ile Lys Gly Lys Val Ile Leu
        35   40   45

atg aga agc aat gtt ttg gat ttc act gaa ttt cat tcc aat ctt ctt   192
Met Arg Ser Asn Val Leu Asp Phe Thr Glu Phe His Ser Asn Leu Leu
    50   55   60

gat aac ttc act gag ctc ttg ggt ggt ggt gtt tct ttc caa ctc att   240
Asp Asn Phe Thr Glu Leu Leu Gly Gly Gly Val Ser Phe Gln Leu Ile
65   70   75   80

agt gcc act cat act tca aat gac tca aga ggg aaa gtt ggg aac aag   288
Ser Ala Thr His Thr Ser Asn Asp Ser Arg Gly Lys Val Gly Asn Lys
                85   90   95

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gca tat ttg gag agg tgg cta act tca atc cca cca ctg ttt gct gga    336
Ala Tyr Leu Glu Arg Trp Leu Thr Ser Ile Pro Pro Leu Phe Ala Gly
            100             105             110

gaa tca gtg ttc caa atc aac ttt caa tgg gat gaa aat ttt gga ttt    384
Glu Ser Val Phe Gln Ile Asn Phe Gln Trp Asp Glu Asn Phe Gly Phe
            115             120             125

cca gga gct ttc ttc ata aaa aat gga cat aca agt gaa ttc ttt ctc    432
Pro Gly Ala Phe Phe Ile Lys Asn Gly His Thr Ser Glu Phe Phe Leu
        130             135             140

aaa tct ctc act ctt gat gat gtt cct ggc tat ggc aga gtc cat ttt    480
Lys Ser Leu Thr Leu Asp Asp Val Pro Gly Tyr Gly Arg Val His Phe
145             150             155             160

gat tgc aat tct tgg gtt tac cct tct gga aga tac aag aaa gat cgc    528
Asp Cys Asn Ser Trp Val Tyr Pro Ser Gly Arg Tyr Lys Lys Asp Arg
                165             170             175

att ttc ttt gcc aat cat gtt tat ctt cca agt caa aca cca aac cct    576
Ile Phe Phe Ala Asn His Val Tyr Leu Pro Ser Gln Thr Pro Asn Pro
            180             185             190

ctt cgt aag tat aga gag gaa gaa ttg tgg aat ttg aga gga gat gga    624
Leu Arg Lys Tyr Arg Glu Glu Glu Leu Trp Asn Leu Arg Gly Asp Gly
            195             200             205

aca gga gaa aga aag gaa tgg gat aga att tat gac tat gat gtt tat    672
Thr Gly Glu Arg Lys Glu Trp Asp Arg Ile Tyr Asp Tyr Asp Val Tyr
    210             215             220

aat gac att gct gac cct gat gtt ggt gat cat cgt cct att ctc ggt    720
Asn Asp Ile Ala Asp Pro Asp Val Gly Asp His Arg Pro Ile Leu Gly
225             230             235             240

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Gly Thr Thr Glu
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            20             25              30
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Arg Val S r Ser Leu Gly Gly Asn Lys Ile Lys Gly Lys Val Ile Leu
        35   40   45

Met Arg Ser Asn Val Leu Asp Phe Thr Glu Phe His Ser Asn Leu Leu
    50   55   60

Asp Asn Phe Thr Glu Leu Leu Gly Gly Gly Val Ser Phe Gln Leu Ile
65   70   75   80

Ser Ala Thr His Thr Ser Asn Asp Ser Arg Gly Lys Val Gly Asn Lys
                85   90   95

Ala Tyr Leu Glu Arg Trp Leu Thr Ser Ile Pro Pro Leu Phe Ala Gly
            100   105   110

Glu Ser Val Phe Gln Ile Asn Phe Gln Trp Asp Glu Asn Phe Gly Phe
        115   120   125

Pro Gly Ala Phe Phe Ile Lys Asn Gly His Thr Ser Glu Phe Phe Leu
    130   135   140

Lys Ser Leu Thr Leu Asp Asp Val Pro Gly Tyr Gly Arg Val His Phe
145   150   155   160

Asp Cys Asn Ser Trp Val Tyr Pro Ser Gly Arg Tyr Lys Lys Asp Arg
                165   170   175

Ile Phe Phe Ala Asn His Val Tyr Leu Pro Ser Gln Thr Pro Asn Pro
            180   185   190

Leu Arg Lys Tyr Arg Glu Glu Glu Leu Trp Asn Leu Arg Gly Asp Gly
        195   200   205

Thr Gly Glu Arg Lys Glu Trp Asp Arg Ile Tyr Asp Tyr Asp Val Tyr
    210   215   220

Asn Asp Ile Ala Asp Pro Asp Val Gly Asp His Arg Pro Ile Leu Gly
225   230   235   240

Gly Thr Thr Glu

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<222> (48)..(2684)

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                                                     1

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Ile Gly Lys Asn Ile Ile Glu Gly Ala Leu Asn Thr Thr Gly Asp Leu
     5   10   15

gca ggt tct gtt atc aat gct ggt ggt aac att tta gat aga gtt tcc   152
Ala Gly Ser Val Ile Asn Ala Gly Gly Asn Ile Leu Asp Arg Val Ser
20   25   30   35

agt ctt gga gga aac aaa atc aaa ggg aaa gtg att ctt atg aga agc   200
Ser Leu Gly Gly Asn Lys Ile Lys Gly Lys Val Ile Leu Met Arg Ser
                40   45   50

aat gtt ttg gat ttc act gaa ttt cat tcc aat ctt ctt gat aac ttc   248
Asn Val Leu Asp Phe Thr Glu Phe His Ser Asn Leu Leu Asp Asn Phe
          55   60   65

act gag ctc ttg ggt ggt ggt gtt tct ttc caa ctc att agt gcc act   296
Thr Glu Leu Leu Gly Gly Gly Val Ser Phe Gln Leu Ile Ser Ala Thr
         70   75   80

cat act tca aat gac tca aga ggg aaa gtt ggg aac aag gca tat ttg   344
His Thr Ser Asn Asp Ser Arg Gly Lys Val Gly Asn Lys Ala Tyr Leu
    85   90   95

gag agg tgg cta act tca atc cca cca ctg ttt gct gga gaa tca gtg   392
Glu Arg Trp Leu Thr Ser Ile Pro Pro Leu Phe Ala Gly Glu Ser Val
100   105   110   115

ttc caa atc aac ttt caa tgg gat gaa aat ttt gga ttt cca gga gct   440
Phe Gln Ile Asn Phe Gln Trp Asp Glu Asn Phe Gly Phe Pro Gly Ala
             120   125   130

ttc ttc ata aaa aat gga cat aca agt gaa ttc ttt ctc aaa tct ctc   488
Phe Phe Ile Lys Asn Gly His Thr Ser Glu Phe Phe Leu Lys Ser Leu
         135   140   145

act ctt gat gat gtt cct ggc tat ggc aga gtc cat ttt gat tgc aat   536
Thr Leu Asp Asp Val Pro Gly Tyr Gly Arg Val His Phe Asp Cys Asn
         150   155   160

tct tgg gtt tac cct tct gga aga tac aag aaa gat cgc att ttc ttt   584
Ser Trp Val Tyr Pro Ser Gly Arg Tyr Lys Lys Asp Arg Ile Phe Phe
         165   170   175

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gcc aat cat gtt tat ctt cca agt caa aca cca aac cct ctt cgt aag    632
Ala Asn His Val Tyr Leu Pro Ser Gln Thr Pro Asn Pro Leu Arg Lys
180             185             190             195

tat aga gag gaa gaa ttg tgg aat ttg aga gga gat gga aca gga gaa    680
Tyr Arg Glu Glu Glu Leu Trp Asn Leu Arg Gly Asp Gly Thr Gly Glu
                200             205             210

aga aag gaa tgg gat aga att tat gac tat gat gtt tat aat gac att    728
Arg Lys Glu Trp Asp Arg Ile Tyr Asp Tyr Asp Val Tyr Asn Asp Ile
            215             220             225

gct gac cct gat gtt ggt gat cat cgt cct att ctc ggt ggg acg acc    776
Ala Asp Pro Asp Val Gly Asp His Arg Pro Ile Leu Gly Gly Thr Thr
        230             235             240

gaa tat cct tac cct cgt agg gga aga aca gga cga cca cga tca aga    824
Glu Tyr Pro Tyr Pro Arg Arg Gly Arg Thr Gly Arg Pro Arg Ser Arg
    245             250             255

aga gac cac aat tat gag agc aga ttg tca cca ata atg agc tta gac    872
Arg Asp His Asn Tyr Glu Ser Arg Leu Ser Pro Ile Met Ser Leu Asp
260             265             270             275

atc tat gta cca aaa gat gaa aac ttt ggg cat ttg aag atg tca gat    920
Ile Tyr Val Pro Lys Asp Glu Asn Phe Gly His Leu Lys Met Ser Asp
                280             285             290

ttc ctt ggt tat aca tta aaa gca ctt tcg ata tca atc aaa cca gga    968
Phe Leu Gly Tyr Thr Leu Lys Ala Leu Ser Ile Ser Ile Lys Pro Gly
            295             300             305

ctt caa tcc ata ttt gat gta act cca aat gaa ttt gac aat ttt aaa    1016
Leu Gln Ser Ile Phe Asp Val Thr Pro Asn Glu Phe Asp Asn Phe Lys
        310             315             320

gaa gtt gat aat ctc ttt gag aga ggt ttt ccc att cca ttt aat gct    1064
Glu Val Asp Asn Leu Phe Glu Arg Gly Phe Pro Ile Pro Phe Asn Ala
        325             330             335

ttt aag acc ctc act gag gac ctc act cca cct ttg ttc aaa gca ctc    1112
Phe Lys Thr Leu Thr Glu Asp Leu Thr Pro Pro Leu Phe Lys Ala Leu
340             345             350             355

gtg agg aat gat ggt gaa aaa ttc ctc aaa ttt cct act ccc gaa gtt    1160
Val Arg Asn Asp Gly Glu Lys Phe Leu Lys Phe Pro Thr Pro Glu Val
                360             365             370

gtc aaa gat aat aaa ata gga tgg agc act gat gaa gaa ttt gca aga    1208
Val Lys Asp Asn Lys Ile Gly Trp Ser Thr Asp Glu Glu Phe Ala Arg
            375             380             385
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gaa atg tta gca gga ccc aat cct cta ttg att cgt cgt ctt gaa gct    1256
Glu Met Leu Ala Gly Pro Asn Pro Leu Leu Ile Arg Arg Leu Glu Ala
        390                 395                 400

ttt cca cca aca agt aag ctt gac cca aat gtt tat ggg aat caa aac    1304
Phe Pro Pro Thr Ser Lys Leu Asp Pro Asn Val Tyr Gly Asn Gln Asn
        405                 410                 415

agt acc atc act gaa gaa cac ata aag cat ggt tta gat ggt ctt acg    1352
Ser Thr Ile Thr Glu Glu His Ile Lys His Gly Leu Asp Gly Leu Thr
420                 425                 430                 435

gtt gat gag gca atg aag caa aac agg ctc tac ata gtg gat ttc cat    1400
Val Asp Glu Ala Met Lys Gln Asn Arg Leu Tyr Ile Val Asp Phe His
                440                 445                 450

gat gca tta atg ccc tat ctt aca agg atg aat gca aca tca aca aaa    1448
Asp Ala Leu Met Pro Tyr Leu Thr Arg Met Asn Ala Thr Ser Thr Lys
                455                 460                 465

aca tat gcc aca aga aca ttg ctt ctt ttg aaa gat gat ggg act ttg    1496
Thr Tyr Ala Thr Arg Thr Leu Leu Leu Leu Lys Asp Asp Gly Thr Leu
                470                 475                 480

aag cca ttg gtt att gag tta gcc ttg cca cat cct caa gga gat caa    1544
Lys Pro Leu Val Ile Glu Leu Ala Leu Pro His Pro Gln Gly Asp Gln
        485                 490                 495

ctt ggt gcc att agc aaa cta tac ttt cca gct gaa aat gga gtt caa    1592
Leu Gly Ala Ile Ser Lys Leu Tyr Phe Pro Ala Glu Asn Gly Val Gln
500                 505                 510                 515

aaa tcc att tgg caa ttg gct aaa gct tat gta act gtt aat gat gtt    1640
Lys Ser Ile Trp Gln Leu Ala Lys Ala Tyr Val Thr Val Asn Asp Val
                520                 525                 530

ggc tac cat caa ctt att agt cat tgg ttg cat act cat gct gta ctt    1688
Gly Tyr His Gln Leu Ile Ser His Trp Leu His Thr His Ala Val Leu
                535                 540                 545

gag cca ttt gtg att gca aca cat aga caa ttg agc gtg ctt cat cca    1736
Glu Pro Phe Val Ile Ala Thr His Arg Gln Leu Ser Val Leu His Pro
        550                 555                 560

atc cat aag ttg ctt gtt cct cat tac aaa gac act atg ttt ata aat    1784
Ile His Lys L u L u Val Pro His Tyr Lys Asp Thr M t Phe Ile Asn
565                 570                 575

gca tct gca aga caa gtt ttg atc aat gcc aat ggt ctt atc gaa aca    1832
Ala Ser Ala Arg Gln Val Leu Ile Asn Ala Asn Gly Leu Ile Glu Thr
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580				585				590				595		

acc cat tat cca tca aaa tat tca atg gag ttg tca tct atc ttg tac   1880
Thr His Tyr Pro Ser Lys Tyr Ser Met Glu Leu Ser Ser Ile Leu Tyr
              600   605   610

aag gat tgg acc ttc cct gat caa gca tta cct aat aat ctc atg aag   1928
Lys Asp Trp Thr Phe Pro Asp Gln Ala Leu Pro Asn Asn Leu Met Lys
            615   620   625

aga gga cta gct gtg gag gac tca agt gcc ccc cat gga ctt aga ttg   1976
Arg Gly Leu Ala Val Glu Asp Ser Ser Ala Pro His Gly Leu Arg Leu
        630   635   640

cta ata aat gat tat cca ttt gct gtt gat ggt ctt gac att tgg tca   2024
Leu Ile Asn Asp Tyr Pro Phe Ala Val Asp Gly Leu Asp Ile Trp Ser
        645   650   655

gcc att aaa aca tgg gta cag gat tat tgc tgt ctc tac tac aaa gat   2072
Ala Ile Lys Thr Trp Val Gln Asp Tyr Cys Cys Leu Tyr Tyr Lys Asp
660   665   670   675

gac aat gca gta caa aat gac ttt gaa ctc caa tct tgg tgg aat gag   2120
Asp Asn Ala Val Gln Asn Asp Phe Glu Leu Gln Ser Trp Trp Asn Glu
            680   685   690

cta aga gag aaa ggc cac gct gac aag aaa cat gaa cca tgg tgg cca   2168
Leu Arg Glu Lys Gly His Ala Asp Lys Lys His Glu Pro Trp Trp Pro
            695   700   705

aaa atg caa act tta agt gaa tta atc gaa tcc tgc act aca att ata   2216
Lys Met Gln Thr Leu Ser Glu Leu Ile Glu Ser Cys Thr Thr Ile Ile
            710   715   720

tgg att gct tca gct ctt cat gcc gca gtt aac ttt gga caa tat ccc   2264
Trp Ile Ala Ser Ala Leu His Ala Ala Val Asn Phe Gly Gln Tyr Pro
        725   730   735

tac gga ggc tat att ctc aat cga cca act aca agt cgt agg ttc atg   2312
Tyr Gly Gly Tyr Ile Leu Asn Arg Pro Thr Thr Ser Arg Arg Phe Met
740   745   750   755

cct gaa gtt ggc acg gct gag tac aaa gaa ctg gaa tcg aat ccc gaa   2360
Pro Glu Val Gly Thr Ala Glu Tyr Lys Glu Leu Glu Ser Asn Pro Glu
            760   765   770

aaa gct ttc ttg aga aca ata tgt tca gaa tta caa gca ctt gtt agt   2408
Lys Ala Ph Leu Arg Thr Il Cys Ser Glu Leu Gln Ala Leu Val Ser
        775   780   785

att tca att att gaa atc ttg tca aag cat gct tct gat gaa gtt tat   2456

Ile S r Ile Ile Glu Ile Leu Ser Lys His Ala Ser Asp Glu Val Tyr
    790   795   800

ctt gga caa aga gct tca att gat tgg act tca gat aaa att gca ttg   2504
Leu Gly Gln Arg Ala Ser Ile Asp Trp Thr Ser Asp Lys Ile Ala Leu
    805   810   815

gaa gca ttt gag aaa ttt ggg aaa aat tta ttt gaa gtt gag aat agg   2552
Glu Ala Phe Glu Lys Phe Gly Lys Asn Leu Phe Glu Val Glu Asn Arg
820   825   830   835

atc atg gaa agg aat aaa gag gtg aat ttg aag aat aga tct gga cct   2600
Ile Met Glu Arg Asn Lys Glu Val Asn Leu Lys Asn Arg Ser Gly Pro
          840   845   850

gtt aat ttg cct tat act cta ctt gtt cca tca agt aac gaa gga ctc   2648
Val Asn Leu Pro Tyr Thr Leu Leu Val Pro Ser Ser Asn Glu Gly Leu
         855   860   865

act gga aga gga att cct aat agt att tct atc taa gttgataaga   2694
Thr Gly Arg Gly Ile Pro Asn Ser Ile Ser Ile
        870   875

aagaaaagtg gttcttttta tgggtgacgt gtgtaatttg aaggtcacaa attacatttt 2754

aagttgccca cattattatt atgaaggaaa taaatgacca tattttagt ttaatttaaa 2814

ttaggtagct atagccaact ttaggctctg ttggatttgg aactatctcc aacttatata 2874

tgtactttgt actactattt gatgaataaa agttgtgtgt cttaagaata aaaaaaaaaa 2934

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<213> Cucumis sativus

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        20   25   30

Arg Val Ser Ser Leu Gly Gly Asn Lys Ile Lys Gly Lys Val Ile Leu
      35   40   45

Met Arg Ser Asn Val Leu Asp Phe Thr Glu Phe His Ser Asn Leu Leu
    50   55   60

Asp Asn Ph Thr Glu Leu L u Gly Gly Gly Val Ser Phe Gln Leu Ile
65   70   75   80

Ser Ala Thr His Thr Ser Asn Asp Ser Arg Gly Lys Val Gly Asn Lys
                    85   90   95

Ala Tyr Leu Glu Arg Trp Leu Thr Ser Ile Pro Pro Leu Phe Ala Gly
                100   105   110

Glu Ser Val Phe Gln Ile Asn Phe Gln Trp Asp Glu Asn Phe Gly Phe
            115   120   125

Pro Gly Ala Phe Phe Ile Lys Asn Gly His Thr Ser Glu Phe Phe Leu
    130   135   140

Lys Ser Leu Thr Leu Asp Asp Val Pro Gly Tyr Gly Arg Val His Phe
145   150   155   160

Asp Cys Asn Ser Trp Val Tyr Pro Ser Gly Arg Tyr Lys Lys Asp Arg
                165   170   175

Ile Phe Phe Ala Asn His Val Tyr Leu Pro Ser Gln Thr Pro Asn Pro
                180   185   190

Leu Arg Lys Tyr Arg Glu Glu Glu Leu Trp Asn Leu Arg Gly Asp Gly
        195   200   205

Thr Gly Glu Arg Lys Glu Trp Asp Arg Ile Tyr Asp Tyr Asp Val Tyr
    210   215   220

Asn Asp Ile Ala Asp Pro Asp Val Gly Asp His Arg Pro Ile Leu Gly
225   230   235   240

Gly Thr Thr Glu Tyr Pro Tyr Pro Arg Arg Gly Arg Thr Gly Arg Pro
            245   250   255

Arg Ser Arg Arg Asp His Asn Tyr Glu Ser Arg Leu Ser Pro Ile Met
        260   265   270

Ser Leu Asp Ile Tyr Val Pro Lys Asp Glu Asn Phe Gly His Leu Lys
    275   280   285

Met Ser Asp Phe Leu Gly Tyr Thr Leu Lys Ala Leu Ser Ile Ser Ile
    290   295   300

Lys Pro Gly Leu Gln Ser Ile Phe Asp Val Thr Pro Asn Glu Phe Asp
305   310   315   320

Asn Phe Lys Glu Val Asp Asn Leu Phe Glu Arg Gly Phe Pro Ile Pro
        325   330   335

Ph Asn Ala Phe Lys Thr L u Thr Glu Asp L u Thr Pro Pro Leu Phe
            340   345   350

Lys Ala Leu Val Arg Asn Asp Gly Glu Lys Phe Leu Lys Phe Pro Thr
        355   360   365

Pro Glu Val Val Lys Asp Asn Lys Ile Gly Trp Ser Thr Asp Glu Glu
    370   375   380

Phe Ala Arg Glu Met Leu Ala Gly Pro Asn Pro Leu Leu Ile Arg Arg
385   390   395   400

Leu Glu Ala Phe Pro Pro Thr Ser Lys Leu Asp Pro Asn Val Tyr Gly
                405   410   415

Asn Gln Asn Ser Thr Ile Thr Glu Glu His Ile Lys His Gly Leu Asp
            420   425   430

Gly Leu Thr Val Asp Glu Ala Met Lys Gln Asn Arg Leu Tyr Ile Val
        435   440   445

Asp Phe His Asp Ala Leu Met Pro Tyr Leu Thr Arg Met Asn Ala Thr
    450   455   460

Ser Thr Lys Thr Tyr Ala Thr Arg Thr Leu Leu Leu Leu Lys Asp Asp
465   470   475   480

Gly Thr Leu Lys Pro Leu Val Ile Glu Leu Ala Leu Pro His Pro Gln
            485   490   495

Gly Asp Gln Leu Gly Ala Ile Ser Lys Leu Tyr Phe Pro Ala Glu Asn
            500   505   510

Gly Val Gln Lys Ser Ile Trp Gln Leu Ala Lys Ala Tyr Val Thr Val
        515   520   525

Asn Asp Val Gly Tyr His Gln Leu Ile Ser His Trp Leu His Thr His
    530   535   540

Ala Val Leu Glu Pro Phe Val Ile Ala Thr His Arg Gln Leu Ser Val
545   550   555   560

Leu His Pro Ile His Lys Leu Leu Val Pro His Tyr Lys Asp Thr Met
            565   570   575

Phe Il Asn Ala Ser Ala Arg Gln Val Leu Ile Asn Ala Asn Gly Leu
            580   585   590

Ile Glu Thr Thr His Tyr Pro Ser Lys Tyr Ser Met Glu Leu Ser Ser
    595   600   605

Ile L u Tyr Lys Asp Trp Thr Ph Pro Asp Gln Ala Leu Pro Asn Asn
610   615   620

Leu Met Lys Arg Gly Leu Ala Val Glu Asp Ser Ser Ala Pro His Gly
625   630   635   640

Leu Arg Leu Leu Ile Asn Asp Tyr Pro Phe Ala Val Asp Gly Leu Asp
             645   650   655

Ile Trp Ser Ala Ile Lys Thr Trp Val Gln Asp Tyr Cys Cys Leu Tyr
      660   665   670

Tyr Lys Asp Asp Asn Ala Val Gln Asn Asp Phe Glu Leu Gln Ser Trp
      675   680   685

Trp Asn Glu Leu Arg Glu Lys Gly His Ala Asp Lys Lys His Glu Pro
     690   695   700

Trp Trp Pro Lys Met Gln Thr Leu Ser Glu Leu Ile Glu Ser Cys Thr
705   710   715   720

Thr Ile Ile Trp Ile Ala Ser Ala Leu His Ala Ala Val Asn Phe Gly
          725   730   735

Gln Tyr Pro Tyr Gly Gly Tyr Ile Leu Asn Arg Pro Thr Thr Ser Arg
         740   745   750

Arg Phe Met Pro Glu Val Gly Thr Ala Glu Tyr Lys Glu Leu Glu Ser
      755   760   765

Asn Pro Glu Lys Ala Phe Leu Arg Thr Ile Cys Ser Glu Leu Gln Ala
    770   775   780

Leu Val Ser Ile Ser Ile Ile Glu Ile Leu Ser Lys His Ala Ser Asp
785   790   795   800

Glu Val Tyr Leu Gly Gln Arg Ala Ser Ile Asp Trp Thr Ser Asp Lys
         805   810   815

Ile Ala Leu Glu Ala Phe Glu Lys Phe Gly Lys Asn Leu Phe Glu Val
         820   825   830

Glu Asn Arg Ile Met Glu Arg Asn Lys Glu Val Asn Leu Lys Asn Arg
      835   840   845

Ser Gly Pro Val Asn Leu Pro Tyr Thr Leu Leu Val Pro S r Ser Asn
    850   855   860

Glu Gly Leu Thr Gly Arg Gly Ile Pro Asn Ser Ile Ser Ile
865   870   875